

RAW SEQUENCE LISTING

The Biotechnology Systems Branch of the Scientific and Technical Information Center (STIC) no errors detected.

Application Serial Number: 10/574,306
Source: JFWP
Date Processed by STIC: 03/13/2007

ENTERED



IFWP

RAW SEQUENCE LISTING
PATENT APPLICATION: US/10/574,306

DATE: 03/13/2007
TIME: 08:29:13

Input Set : A:\50458.002001.txt
Output Set: N:\CRF4\03132007\J574306.raw

3 <110> APPLICANT: Korherr, Christian
 5 <120> TITLE OF INVENTION: Medical Use of TBK-1 or of Inhibitors Thereof
 7 <130> FILE REFERENCE: 50458/002001
 9 <140> CURRENT APPLICATION NUMBER: US 10/574,306
 10 <141> CURRENT FILING DATE: 2006-04-03
 12 <150> PRIOR APPLICATION NUMBER: PCT/EP2004/010996
 13 <151> PRIOR FILING DATE: 2004-10-01
 15 <150> PRIOR APPLICATION NUMBER: US 60/508,100
 16 <151> PRIOR FILING DATE: 2003-10-02
 18 <160> NUMBER OF SEQ ID NOS: 10
 20 <170> SOFTWARE: PatentIn version 3.3
 22 <210> SEQ ID NO: 1
 23 <211> LENGTH: 3031
 24 <212> TYPE: DNA
 25 <213> ORGANISM: Homo sapiens
 27 <400> SEQUENCE: 1
 28 cctcgtgccg aattcgac gaggccgcg ggccgtggcg cggcggagac ccggctggta 60
 30 taacaagagg attgcctgat ccagccaaga tgcagagcac ttctaattcat ctgtggcttt 120
 32 tatctgatat tttaggcca gtagacttgc caaatgtct tcgtggaaata cataagaaaa 180
 34 ctgtgttattt atttgtatc aaagtattta ataacataag cttcccttcgt ccagtggatg 240
 36 ttcaaattttag agaattttagaa gtgttggaaa aactcaatca caaaaatattt gtcaatttat 300
 38 ttgttatttga agaggagaca acaacaagac ataaaatgtact tattatggaa ttttgtccat 360
 40 gtgggagttt atacactgtt tttagaaac cttctaatgc ctatggactt ccagaatctg 420
 42 aattcttaat tggttgcga gatgtggtggtt gttggaaatca tcatctacga gagaatggta 480
 44 tagtgcacccg tgatatacaag ccaggaaata tcatgcgtt tataaggggaa gatggacagt 540
 46 ctgtgtacaa actcacatgat ttgttgcag ctagagaattt agaagatgtt gagcagttt 600
 48 ttctctgtt tggcacagaa gaatatttgc accctgat tttatggaaa gcaatgttca 660
 50 gaaaatca tcagaagaaa tatggagca cagttatct ttggggatc ggggttacat 720
 52 tttaccatgc agtacttgc tcaactgcattt ttagaccctt tgaaggccctt cgttggatata 780
 54 aagaatgtt gtataaaaata attacaggaa agccttctgg tgcaatatctt ggatgtacaga 840
 56 aagcagaaaa tggaccaattt gactggatgtt gagacatgcc ttgttcttc agtcttctc 900
 58 ggggttccca ggttctactt accctgttcc ttgcaaacat ctttgcgttca gatcaggaaa 960
 60 agtgggggggg ttttggccat ttttttgcag aaactgttga tataacttcac cgaatggtaa 1020
 62 ttcatgtttt ttgcgttacaa caaatgtacat ctcataatgtt ttatattcat agtataata 1080
 64 ctgtactat atttcatgaa ctgttatata aacaaacca aattattttt tcaaataatcaag 1140
 66 aacttatcta cgaaggccga cgcttagtct tagaacctgg aaggctggca caacatttcc 1200
 68 ctaaaactac tgaggaaaac cctatatttgc tagtaagccg ggaacctctg aataccatag 1260
 70 gattaatata tgaaaaattt tccctccctt aagtacatcc acgttatgtt ttagacgggg 1320
 72 atgttagcat ggctaaaggca ataacagggg ttgtgtgtt tgcctgcaga attggccatgt 1380
 74 ccttactgtt ttatcaggaa ttaatgcgaa agggatgtt atggctgtt gaattatca 1440
 76 aagatgatta caatgaaact gttcacaaaa agacagaatgtt gttgtatcaca ttggatttct 1500
 78 gtatcagaaaa cattgaaaaactgtgaaatgat tttatgaaaa gttgtatgaaatcaacatgg 1560
 80 aagccgcaga gtttaggttca atttcagaca tacacaccaat ttttttttttccatgtt 1620

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82	ctcagggAAC	aatagAAACC	agtCTTCAGG	atATCGACAG	cAGATTATCT	ccAGGTGGAT	1680
84	caCTGGCAGA	cgCATGGGCA	catCAAGAAG	gcACTCATCC	gaaAGACAGA	aatGTAGAAA	1740
86	aactacaAGT	cctgttaAT	tgcATGACAG	agattTACTA	tcaGTTAAA	aaAGACAAAG	1800
88	cagaACGTAG	attagCTTAT	aatGAAGAAC	aaATCCACAA	atttgATAAG	caAAAACtGT	1860
90	attaccatGC	cacAAAGCT	atgACGCACT	ttACAGATGA	atgtGTAA	aAGTATGAGG	1920
92	cattttGAA	taAGTCAGAA	gaATGGATAA	gaaAGATGCT	tcaTCTTAGG	aaACAGTTAT	1980
94	tatCgCTGAC	taatCAGTGT	tttGATATTG	aAGAAGAAGT	atCAAAATAT	caAGAAATA	2040
96	ctaAtGAGTT	acaAGAAACT	ctgcCTCAGA	aaATGTTAC	agCTTCCAGT	ggaATCAAAC	2100
98	ataccatGAC	cccAATTAT	ccaAGTTCTA	acACATTAGT	agAAATGACT	cttGGTATGA	2160
100	agaaaATTAAA	ggaAGAGATG	gaAGGGGTGG	ttaAGAACT	tgCTGAAAAT	aACCACATT	2220
102	tagAAAGGT	tggCTTTA	accATGGATG	gtggCCTCG	caACGTTGAC	tgtCTTAgC	2280
104	tttCTAATAG	aAGTTAAGA	aaAGTTCCG	tttgcACAAG	aaaATAACGC	ttggcATTA	2340
106	aatGAATGCC	tttATAGATA	gtCACTTGT	tctACAATT	agtATTGAT	gtggCgtGT	2400
108	aaATATGTAC	aatATTGTA	atACATAAAA	aatATACAAA	ttttGGCTG	ctgtGAAGAT	2460
110	gtAAATTAT	ctttAAACAT	ttATAATTAT	atGAGGAAT	ttGACCTCAG	tgtCACGAG	2520
112	aagAAAGCCA	tgaccGACCA	atATGTTGAC	atACTGATCC	tctACTCTGA	gtggggCTAA	2580
114	ataAGTTATT	ttctCTGACC	gcCTACTGGA	aatATTTTA	agtGGAACCA	aaATAGGCA	2640
116	ccttACAAAT	cAGGAAGACT	gACTTGACAC	gtttGTAAT	ggtGAACGG	tggCTACTGT	2700
118	gagtGGGGAG	cagaACCGCA	ccACTGTTAT	actGGGATAA	caATTTTTT	gagaAGGATA	2760
120	aagtGGCATT	atTTTATTT	acaAGGTGCC	cAGATCCCAG	ttATCCTGT	atCCATGTAA	2820
122	tttCAGATGA	attATTAAGC	aaACATT	aAGTGAATT	attATTA	aaACTATT	2880
124	ttttCCTT	ggCCATAAAAT	gtGTAATTG	cattAAATT	ctAAGGTCA	ttCAACTGTT	2940
126	ttaAGCTGTA	tATTTCTTA	attCTGCTA	ctATTCA	gaaaaAAATA	aATTCTCAA	3000
128	tttTAATGTA	aAGAAAAAAA	aaaaAAA	a			3031

131 <210> SEQ ID NO: 2

132 <211> LENGTH: 729

133 <212> TYPE: PRT

134 <213> ORGANISM: Homo sapiens

136 <400> SEQUENCE: 2

138	Met	Gln	Ser	Thr	Ser	Asn	His	Leu	Trp	Leu	Leu	Ser	Asp	Ile	Leu	Gly
139	1						5				10					15
142	Gln	Gly	Ala	Thr	Ala	Asn	Val	Phe	Arg	Gly	Arg	His	Lys	Lys	Thr	Gly
143							20				25					30
146	Asp	Leu	Phe	Ala	Ile	Lys	Val	Phe	Asn	Asn	Ile	Ser	Phe	Leu	Arg	Pro
147							35				40					45
150	Val	Asp	Val	Gln	Met	Arg	Glu	Phe	Glu	Val	Leu	Lys	Lys	Leu	Asn	His
151							50				55					60
154	Lys	Asn	Ile	Val	Lys	Leu	Phe	Ala	Ile	Glu	Glu	Glu	Thr	Thr	Thr	Arg
155							65				70					80
158	His	Lys	Val	Leu	Ile	Met	Glu	Phe	Cys	Pro	Cys	Gly	Ser	Leu	Tyr	Thr
159							85				90					95
162	Val	Leu	Glu	Glu	Pro	Ser	Asn	Ala	Tyr	Gly	Leu	Pro	Glu	Ser	Glu	Phe
163							100				105					110
166	Leu	Ile	Val	Leu	Arg	Asp	Val	Val	Gly	Gly	Met	Asn	His	Leu	Arg	Glu
167							115				120					125
170	Asn	Gly	Ile	Val	His	Arg	Asp	Ile	Lys	Pro	Gly	Asn	Ile	Met	Arg	Val
171							130				135					140
174	Ile	Gly	Glu	Asp	Gly	Gln	Ser	Val	Tyr	Lys	Leu	Thr	Asp	Phe	Gly	Ala
175							145				150					160
											155					

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178 Ala Arg Glu Leu Glu Asp Asp Glu Gln Phe Val Ser Leu Tyr Gly Thr
179 165 170 175
182 Glu Glu Tyr Leu His Pro Asp Met Tyr Glu Arg Ala Val Leu Arg Lys
183 180 185 190
186 Asp His Gln Lys Lys Tyr Gly Ala Thr Val Asp Leu Trp Ser Ile Gly
187 195 200 205
190 Val Thr Phe Tyr His Ala Ala Thr Gly Ser Leu Pro Phe Arg Pro Phe
191 210 215 220
194 Glu Gly Pro Arg Arg Asn Lys Glu Val Met Tyr Lys Ile Ile Thr Gly
195 225 230 235 240
198 Lys Pro Ser Gly Ala Ile Ser Gly Val Gln Lys Ala Glu Asn Gly Pro
199 245 250 255
202 Ile Asp Trp Ser Gly Asp Met Pro Val Ser Cys Ser Leu Ser Arg Gly
203 260 265 270
206 Leu Gln Val Leu Leu Thr Pro Val Leu Ala Asn Ile Leu Glu Ala Asp
207 275 280 285
210 Gln Glu Lys Cys Trp Gly Phe Asp Gln Phe Phe Ala Glu Thr Ser Asp
211 290 295 300
214 Ile Leu His Arg Met Val Ile His Val Phe Ser Leu Gln Gln Met Thr
215 305 310 315 320
218 Ala His Lys Ile Tyr Ile His Ser Tyr Asn Thr Ala Thr Ile Phe His
219 325 330 335
222 Glu Leu Val Tyr Lys Gln Thr Lys Ile Ile Ser Ser Asn Gln Glu Leu
223 340 345 350
226 Ile Tyr Glu Gly Arg Arg Leu Val Leu Glu Pro Gly Arg Leu Ala Gln
227 355 360 365
230 His Phe Pro Lys Thr Thr Glu Glu Asn Pro Ile Phe Val Val Ser Arg
231 370 375 380
234 Glu Pro Leu Asn Thr Ile Gly Leu Ile Tyr Glu Lys Ile Ser Leu Pro
235 385 390 395 400
238 Lys Val His Pro Arg Tyr Asp Leu Asp Gly Asp Ala Ser Met Ala Lys
239 405 410 415
242 Ala Ile Thr Gly Val Val Cys Tyr Ala Cys Arg Ile Ala Ser Thr Leu
243 420 425 430
246 Leu Leu Tyr Gln Glu Leu Met Arg Lys Gly Ile Arg Trp Leu Ile Glu
247 435 440 445
250 Leu Ile Lys Asp Asp Tyr Asn Glu Thr Val His Lys Lys Thr Glu Val
251 450 455 460
254 Val Ile Thr Leu Asp Phe Cys Ile Arg Asn Ile Glu Lys Thr Val Lys
255 465 470 475 480
258 Val Tyr Glu Lys Leu Met Lys Ile Asn Leu Glu Ala Ala Glu Leu Gly
259 485 490 495
262 Glu Ile Ser Asp Ile His Thr Lys Leu Leu Arg Leu Ser Ser Ser Gln
263 500 505 510
266 Gly Thr Ile Glu Thr Ser Leu Gln Asp Ile Asp Ser Arg Leu Ser Pro
267 515 520 525
270 Gly Gly Ser Leu Ala Asp Ala Trp Ala His Gln Glu Gly Thr His Pro
271 530 535 540
274 Lys Asp Arg Asn Val Glu Lys Leu Gln Val Leu Leu Asn Cys Met Thr

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275	545	550	555	560
278	Glu Ile Tyr Tyr Gln Phe Lys Lys Asp Lys Ala Glu Arg Arg Leu Ala			
279	565	570	575	
282	Tyr Asn Glu Glu Gln Ile His Lys Phe Asp Lys Gln Lys Leu Tyr Tyr			
283	580	585	590	
286	His Ala Thr Lys Ala Met Thr His Phe Thr Asp Glu Cys Val Lys Lys			
287	595	600	605	
290	Tyr Glu Ala Phe Leu Asn Lys Ser Glu Glu Trp Ile Arg Lys Met Leu			
291	610	615	620	
294	His Leu Arg Lys Gln Leu Leu Ser Leu Thr Asn Gln Cys Phe Asp Ile			
295	625	630	635	640
298	Glu Glu Glu Val Ser Lys Tyr Gln Glu Tyr Thr Asn Glu Leu Gln Glu			
299	645	650	655	
302	Thr Leu Pro Gln Lys Met Phe Thr Ala Ser Ser Gly Ile Lys His Thr			
303	660	665	670	
306	Met Thr Pro Ile Tyr Pro Ser Ser Asn Thr Leu Val Glu Met Thr Leu			
307	675	680	685	
310	Gly Met Lys Lys Leu Lys Glu Glu Met Glu Gly Val Val Lys Glu Leu			
311	690	695	700	
314	Ala Glu Asn Asn His Ile Leu Glu Arg Phe Gly Ser Leu Thr Met Asp			
315	705	710	715	720
318	Gly Gly Leu Arg Asn Val Asp Cys Leu			
319	725			
322	<210> SEQ ID NO: 3			
323	<211> LENGTH: 19			
324	<212> TYPE: RNA			
325	<213> ORGANISM: artificial			
327	<220> FEATURE:			
328	<223> OTHER INFORMATION: oligonucleotide siTBK-1 sense			
330	<400> SEQUENCE: 3			
331	ggagacaaca acaagacau		19	
334	<210> SEQ ID NO: 4			
335	<211> LENGTH: 20			
336	<212> TYPE: RNA			
337	<213> ORGANISM: artificial			
339	<220> FEATURE:			
340	<223> OTHER INFORMATION: oligonucleotide siTBK-1 antisense			
342	<400> SEQUENCE: 4			
343	augucuuguu guugucucc		20	
346	<210> SEQ ID NO: 5			
347	<211> LENGTH: 23			
348	<212> TYPE: DNA			
349	<213> ORGANISM: artificial			
351	<220> FEATURE:			
352	<223> OTHER INFORMATION: oligonucleotide TBK-1 sense			
354	<400> SEQUENCE: 5			
355	ttgaagagga gacaacaaca aga		23	
358	<210> SEQ ID NO: 6			
359	<211> LENGTH: 19			

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Input Set : A:\50458.002001.txt
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360 <212> TYPE: DNA
361 <213> ORGANISM: artificial
363 <220> FEATURE:
364 <223> OTHER INFORMATION: oligonucleotide TBK-1 antisense
366 <400> SEQUENCE: 6
367 cattccaccc accacatct 19
370 <210> SEQ ID NO: 7
371 <211> LENGTH: 20
372 <212> TYPE: DNA
373 <213> ORGANISM: artificial
375 <220> FEATURE:
376 <223> OTHER INFORMATION: oligonucleotide VEGF sense
378 <400> SEQUENCE: 7
379 ctgcgccttgc tgctctacct 20
382 <210> SEQ ID NO: 8
383 <211> LENGTH: 20
384 <212> TYPE: DNA
385 <213> ORGANISM: artificial
387 <220> FEATURE:
388 <223> OTHER INFORMATION: oligonucleotide VEGF antisense
390 <400> SEQUENCE: 8
391 gattctgccc tcctccttct 20
394 <210> SEQ ID NO: 9
395 <211> LENGTH: 20
396 <212> TYPE: DNA
397 <213> ORGANISM: artificial
399 <220> FEATURE:
400 <223> OTHER INFORMATION: oligonucleotide Rantes sense
402 <400> SEQUENCE: 9
403 cgctgtcatac ctcattgcta 20
406 <210> SEQ ID NO: 10
407 <211> LENGTH: 20
408 <212> TYPE: DNA
409 <213> ORGANISM: artificial
411 <220> FEATURE:
412 <223> OTHER INFORMATION: oligonucleotide Rantes antisense
414 <400> SEQUENCE: 10
415 gcacttgcca ctggtgtaga 20

RAW SEQUENCE LISTING ERROR SUMMARY
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Input Set : A:\50458.002001.txt
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Invalid <213> Response:

Use of "Artificial" only as "<213> Organism" response is incomplete,
per 1.823(b) of New Sequence Rules. Valid response is Artificial Sequence.

Seq#:3,4,5,6,7,8,9,10

VERIFICATION SUMMARY

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